

Applicants:  
Application No.:  
For:  
Agent:

Bruce D. Cohen et al.  
To Be Assigned  
ANTIBODIES TO INSULIN-LIKE GROWTH  
FACTOR I RECEPTOR  
Karen E. Brown, Reg. No. 43,866

Docket No.: ABX-PF2 US  
Filed: Herewith

Express Mail No.  
EL 889410403 US

2.13.2K	GACATCCAGA	TGACCCAGTT	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
A30	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
2.14.3K	-----	-----	----TCCTCC	CTGTCTGCAT	CTGTAGGAGA	26
2.12.1K	-----	-----	-----	-----TGCAT	CTGTAGGAGA	15
4.9.2K	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTY	TCCATCCTCC	CTGTCTGCAT	CTGTAGGAGA	50

CDR1

2.13.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AATGATTTAG	100
A30	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AATGATTTAG	100
2.14.3K	CAGAGTCACC	TTCACCTTGCC	GGGCAAGTCA	GGACATTAGA	CGTGATTTAG	76
2.12.1K	CAGAGTCACC	TTCACCTTGCC	GGGCAAGTCA	GGACATTAGA	CGTGATTTAG	65
4.9.2K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GGGCATTAGA	AGTGATTTAG	100
Consensus	CAGAGTCACC	WTCACTTGCC	GGGCAAGTCA	GGGCATTAGA	MRTGATTTAG	100

2.13.2K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
A30	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
2.14.3K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCT	CTAAGCGCCT	GATCTATGCT	126
2.12.1K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCT	CTAAGCGCCT	GATCTATGCT	115
4.9.2K	GCTGGTATCA	GCAGAAACCA	GGGAAAGCC	CTAAGCGCCT	GATCTATGCT	150
Consensus	GCTGGTATCA	GCAGAAACCA	GGGAAAGCT	CTAAGCGCCT	GATCTATGCT	150

CDR2

2.13.2K	GCATCCCGTT	TGCACAGAGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
A30	GCATCCAGTT	TGCACAGTGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
2.14.3K	GCATCCCGTT	TACAAAGTGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	176
2.12.1K	GCATCCCGTT	TACAAAGTGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	165
4.9.2K	GCATCCAAAT	TACACCGTGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	200
Consensus	GCATCCMRWT	TRCAMMGAGG	GGTCCCATCA	AGGTTCAGCG	GCAGTGGATC	200

2.13.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250
A30	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	250
2.14.3K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	226
2.12.1K	TGGGACAGAA	TTCACTCTCA	CAATCAGCAG	CCTGCAGCCT	GAAGATTTTG	215
4.9.2K	TGGGACAGAA	TTCACTCTCA	CAATCAGCCG	CCTGCAGCCT	GAAGATTTTG	250
Consensus	TGGGACAGAA	TTCACTCTCA	CAATCAGCMG	CCTGCAGCCT	GAAGATTTTG	250

CDR3

2.13.2K	CAACTTATTA	CTGTCTACAA	CATAATAGTT	ACCGTGCAG	TTTTGGCCAG	300
A30	CAACTTATTA	CTGTCTACAG	CATAATAGTT	AACC-TCCN-	-----	288
2.14.3K	CAACTTATTA	CTGTCTACAG	CATAATAATT	ATCCTCGGAC	GTTCGGCCAA	276
2.12.1K	CAACTTATTA	CTGTCTACAG	CATAATAATT	ATCCTCGGAC	GTTCGGCCAA	265
4.9.2K	CAACTTATTA	CTGTCTACAG	CATAATAGTT	ACCGTCTCAC	TTTCGGCGGA	300
Consensus	CAACTTATTA	CTGTYTACAR	CATAATARTT	AYCKYBSNS	KTTYGGCSRR	300

2.13.2K	GGGACCAAGC	TGGAGATCAA	AC----	322
A30	-----	-----	-----	288
2.14.3K	GGGACCGAGG	TGGAAATCAT	ACGAAC	302
2.12.1K	GGGACCGAGG	TGGAAATCAT	ACGAAC	291
4.9.2K	GGGACCAAGG	TGGAGATCAA	AC----	322
Consensus	GGGACCRAGS	TGGARATCAW	ACGAAC	326

FIG. 1A

4.17.3K	-----	-----	-----	-----	AGGAGA	7
O12	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC'TGCAT	CTGTAGGAGA	50
Consensus	GACATCCAGA	TGACCCAGTC	TCCATCCTCC	CTGTC'TGCAT	CTGYAGGAGA	50
CDR1						
4.17.3K	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGT	ACCTTTTTAA	57
O12	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGC	AGCTATTTAA	100
Consensus	CAGAGTCACC	ATCACTTGCC	GGGCAAGTCA	GAGCATTAGY	ASCTTTTTAA	100
4.17.3K	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAAACTCCT	GATCCATGTT	107
O12	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAAGCTCCT	GATCTATGCT	150
Consensus	ATTGGTATCA	GCAGAAACCA	GGGAAAGCCC	CTAARCTCCT	GATCYATGYT	150
CDR2						
4.17.3K	GCATCCAGTT	TACAAGGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	157
O12	GCATCCAGTT	TGCAAAAGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
Consensus	GCATCCAGTT	TCCAARGTGG	GGTCCCATCA	AGGTTCAAGT	GCAGTGGATC	200
4.17.3K	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	207
O12	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
Consensus	TGGGACAGAT	TTCACTCTCA	CCATCAGCAG	TCTGCAACCT	GAAGATTTTG	250
CDR3						
4.17.3K	CAACTTACTA	CTGTCAACAG	AGTTACAATG	CCCCACTCAC	TTTCGGCGGA	257
O12	CAACTTACTA	CTGTCAACAG	AGTTACAATA	CCCC-TOCH-	-----	288
Consensus	CAACTTACTA	CTGTCAACAG	AGTTACATR	CCCCAYYCHC	TTTCGGCGGA	300
4.17.3K	GGGACCAAGG	TGGAGATCAA	AC			279
O12	-----	-----	--			288
Consensus	GGGACCAAGG	TGGAGATCAA	AC			322

FIG. 1B

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6.1.1K	-----	-----	-----	-----	-----	50
A27	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	50
Consensus	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	50
	CDR1					
6.1.1K	-AGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTCGC	GGCAGGTACT	49
A27	AAGAGCCACC	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AGCAGCTACT	100
Consensus	AAGAGCCACC	CTCTCCTGTA	GGGCCAGTCA	GAGTGTTCGC	AGCAGGTACT	100
6.1.1K	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	99
A27	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
Consensus	TAGCCTGGTA	CCAGCAGAAA	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	150
	CDR2					
6.1.1K	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	149
A27	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
Consensus	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	GACAGGTTCA	GTGGCAGTGG	200
6.1.1K	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	199
A27	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
Consensus	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	CCTGAAGATT	250
	CDR3					
6.1.1K	TTGCAGTGTT	TTACTGTCAG	CAGTATGGTA	GTTCACCTCG	NACGTTTCGGC	249
A27	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GCTCACCTCC	-----	290
Consensus	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GTCACCTCS	NACGTTTCGGC	300
6.1.1K	CAAGGGACCA	AGGTGGAAAT	CAAAC			274
A27	-----	-----	-----			290
Consensus	CAAGGGACCA	AGGTGGAAAT	CAAAC			325

FIG. 1C

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2.12.1H	-----	-----	---	GGGAGGC	TTGGTCAAGC	CTGGA	GGTC	26
DP35	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGAGGGTC			50
Consensus	CAGGTGCAGC	TGGTGGAGTC	TGGGGGAGGC	TTGGTCAAGC	CTGGAGGGTC			50
CDR1								
2.12.1H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTATA		76
DP35	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTACA		100
Consensus	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CAC	TTTCAGT	GACTACTAYA		100
2.12.1H	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAA	ATG	GGTTTCATAC		126
DP35	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAG	ATG	GGTTTCATAC		150
Consensus	TGAGCTGGAT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAR	ATG	GGTTTCATAC		150
CDR2								
2.12.1H	ATTAGTAGTA	GTGGTAGTAC	CAG	ACTAC	GCAGACTCTG	TGAAGGGCCG		176
DP35	ATTAGTAGTA	GTGGTAGTAC	CAT	ACTAC	GCAGACTCTG	TGAAGGGCCG		200
Consensus	ATTAGTAGTA	GTGGTAGTAC	CAK	ACTAC	GCAGACTCTG	TGAAGGGCCG		200
2.12.1H	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA			226
DP35	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA			250
Consensus	ATTCACCATC	TCCAGGGACA	ACGCCAAGAA	CTCACTGTAT	CTGCAAATGA			250
2.12.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGT	GAGAGATGGA			276
DP35	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGC	GAGAGA----			296
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTGT	ATTACTGTGY	GAGAGATGGA			300
CDR3								
2.12.1H	GTGGAAACTA	CTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA			326
DP35	-----	-----	-----	-----	-----			296
Consensus	GTGGAAACTA	CTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA			350
2.12.1H	AGGGACCACG	GTCACCGTCT	CCTCAG					352
DP35	-----	-----	-----					296
Consensus	AGGGACCACG	GTCACCGTCT	CCTCAG					376

FIG. 2A

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PF2-2.14.3H.DNA	-----	GGGCCAGGA	CTGGTGAAGC	CTTCGGAGAC	30	
VIV-4/4.35	CAGGTGCAGC	TGCAGGAGTC	GGGCCAGGA	CTGGTGAAGC	CTTCGGAGAC	50
Consensus	CAGGTGCAGC	TGCAGGAGTC	GGGCCAGGA	CTGGTGAAGC	CTTCGGAGAC	50
				CDR1		
PF2-2.14.3H.DNA	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	ATTACTACT	80
VIV-4/4.35	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	ATTACTACT	100
Consensus	CCTGTCCCTC	ACCTGCACTG	TCTCTGGTGG	CTCCATCAGT	ATTACTACT	100
	CDR1					
PF2-2.14.3H.DNA	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	GATTGGGCGT	130
VIV-4/4.35	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	GATTGGGCGT	150
Consensus	GGAGCTGGAT	CCGGCAGCCC	GCCGGGAAGG	GACTGGAGTG	GATTGGGCGT	150
		CDR2				
PF2-2.14.3H.DNA	ATCTATACCA	GTGGGAGCC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	180
VIV-4/4.35	ATCTATACCA	GTGGGAGCAC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	200
Consensus	ATCTATACCA	GTGGGAGCC	CAACTACAAC	CCCTCCCTCA	AGAGTCGAGT	200
PF2-2.14.3H.DNA	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAAC	230
VIV-4/4.35	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAGCT	250
Consensus	CACCATGTCA	GTAGACACGT	CCAAGAACCA	GTTCTCCCTG	AAGCTGAAC	250
PF2-2.14.3H.DNA	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGG	T AACGATTTTT	280
VIV-4/4.35	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGG	-----	288
Consensus	CTGTGACCGC	CGCGGACACG	GCCGTGTATT	ACTGTGCGG	T AACGATTTTT	300
		CDR3				
PF2-2.14.3H.DNA	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CAGGGAAACC	TGGTCACCGT	330
VIV-4/4.35	-----	-----	-----	ACAGAB----	-----	294
Consensus	GGAGTGGTTA	TTATCTTTGA	CTACTGGGGC	CAGGGANCC	TGGTCACCGT	350
PF2-2.14.3H.DNA	CTCCTCAG					338
VIV-4/4.35	-----					294
Consensus	CTCCTCAG					358

FIG. 2B

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6.1.1H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
4.9.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
DP47	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
2.13.2H	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
Consensus	GAGGTGCAGC	TGTTGGAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	50
CDR1						
6.1.1H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
4.9.2H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
DP47	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
2.13.2H	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
Consensus	CCTGAGACTC	TCCTGTGCAG	CCTCTGGATT	CACCTTTAGC	AGCTATGCCA	100
CDR1						
6.1.1H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
4.9.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
DP47	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
2.13.2H	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
Consensus	TGAGCTGGGT	CCGCCAGGCT	CCAGGGAAGG	GGCTGGAGTG	GGTCTCAGCT	150
CDR2						
6.1.1H	ATTACTGGGA	GTGGTGGTAG	TACATACTAC	GCAGACTCCG	TGAAGGGCCG	200
4.9.2H	ATTAGTGGTA	GTGGTGGTAT	CACATACTAC	GCAGACTCCG	TGAAGGGCCG	200
DP47	ATTAGTGGTA	GTGGTGGTAG	CACATACTAC	GCAGACTCCG	TGAAGGGCCG	200
2.13.2H	ATTAGTGGTA	GTGGTGGTAC	CACATICTAC	GCAGACTCCG	TGAAGGGCCG	200
Consensus	ATTASTGGKA	GTGGTGGTAB	YACATICTAC	GCAGACTCCG	TGAAGGGCCG	200
CDR3						
6.1.1H	GTTCACCATC	TCCAGAGACA	ATTCCAAGAA	CACGCTGTAT	CTGCAAATGA	250
4.9.2H	GTTCACCATC	TCCAGAGACA	ATTCCAAGAA	CACGCTGTAT	CTGCAAATGA	250
DP47	GTTCACCATC	TCCAGAGACA	ATTCCAAGAA	CACGCTGTAT	CTGCAAATGA	250
2.13.2H	GTTCACCATC	TCCAGAGACA	ATTCCAAGAC	CACGCTGTAT	CTGCAAATGA	250
Consensus	GTTCACCATC	TCCAGAGACA	ATTCCAAGAM	CACGCTGTAT	CTGCAAATGA	250
CDR3						
6.1.1H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATC--	298
4.9.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTG	300
DP47	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGA----	296
2.13.2H	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTT	300
Consensus	ACAGCCTGAG	AGCCGAGGAC	ACGGCCGTAT	ATTACTGTGC	GAAAGATCTK	300
CDR3-for 4.9.2 and 2.13.2						
6.1.1H	-----	-----	-----	-----	-----C-	299
4.9.2H	GGCTACGGTG	ACTTTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
DP47	-----	-----	-----	-----	-----	296
2.13.2H	GGCTGGTCCG	ACTCTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
Consensus	GGCTRSKSYG	ACTYTTACTA	CTACTACTAC	GGTATGGACG	TCTGGGGCCA	350
CDR3-for 6.1.1						
6.1.1H	AGGGACTACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	349
4.9.2H	AGGGACCAC-	-----	-----	-----	-----	359
DP47	-----	-----	-----	-----	-----	296
2.13.2H	AGGGACCAC-	-----	-----	-----	-----	359
Consensus	AGGGACYACG	GTGATTATGA	GTTGGTTCGA	CCCCTGGGGC	CAGGGAACCC	400

FIG. 2C-1

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6.1.1H	TGGTCACCGT CTCCTCAG	367
4.9.2H	-GGTCACCGT CTCCTCAG	376
DP47	-----	296
2.13.2H	-GGTCACCGT CTCCTCAG	376
Consensus	TGGTCACCGT CTCCTCAG	418

FIG. 2C-2

4.17.3H	-----	CCCAGGA CTGGTGAAGC CTTCGGAGAC	27
DP71	CAGGTGCAGC TGCAGGAGTC GGC	CCCAGGA CTGGTGAAGC CTTCGGAGAC	50
Consensus	CAGGTGCAGC TGCAGGAGTC GGC	CCCAGGA CTGGTGAAGC CTTCGGAGAC	50
		CDR1	
4.17.3H	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AGTTACTACT	77
DP71	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AGTTACTACT	100
Consensus	CCTGTCCCTC ACCTGCACTG TCTCTGGTGG CTCCATCAGT	AGTTACTACT	100
		CDR1	
4.17.3H	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG	GATTGGGTAT	127
DP71	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG	GATTGGGTAT	150
Consensus	GGAGTTGGAT CCGGCAGCCC CCAGGGAAGG GACTGGAGTG	GATTGGGTAT	150
		CDR2	
4.17.3H	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA	AGAGTCGAGT	177
DP71	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA	AGAGTCGAGT	200
Consensus	ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA	AGAGTCGAGT	200
4.17.3H	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG	AAGCTGAGCT	227
DP71	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG	AAGCTGAGCT	250
Consensus	CACCATATCA GTAGACACGT CCAAGAACCA GTTCTCCCTG	AAGCTGAGCT	250
		CDR3	
4.17.3H	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGC	CAG GACGTATAGC	277
DP71	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGC	--- GA-----	289
Consensus	CTGTGACCGC TGCGGACACG GCCGTGTATT ACTGTGC	CAG GACGTATAGC	300
4.17.3H	AGTTCGTTCT ACTACTACGG TATG	GACGTC TGGGGCCAAG GGACCACGGT	327
DP71	-----	---GA-----	293
Consensus	AGTTCGTTCT ACTACTACGG TATG	GACGTC TGGGGCCAAG GGACCACGGT	350
4.17.3H	CACCGTCTCC TCAG		341
DP71	-----		293
Consensus	CACCGTCTCC TCAG		364

FIG. 2D

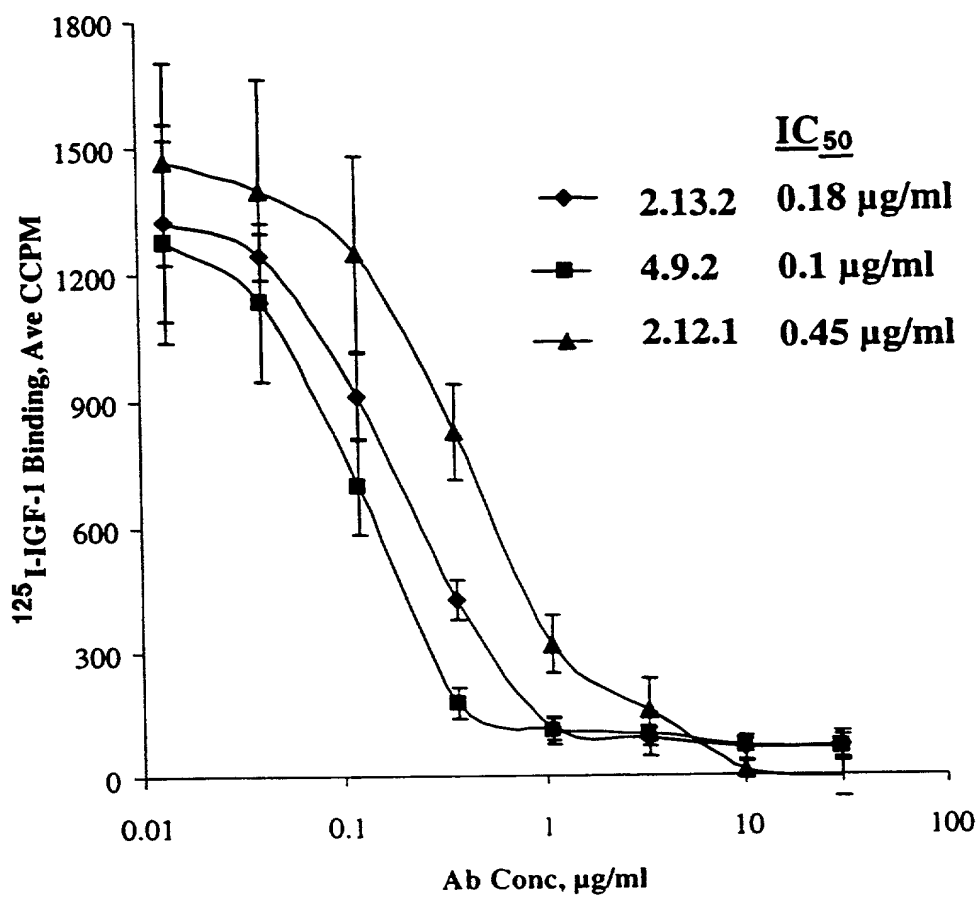


FIG. 3



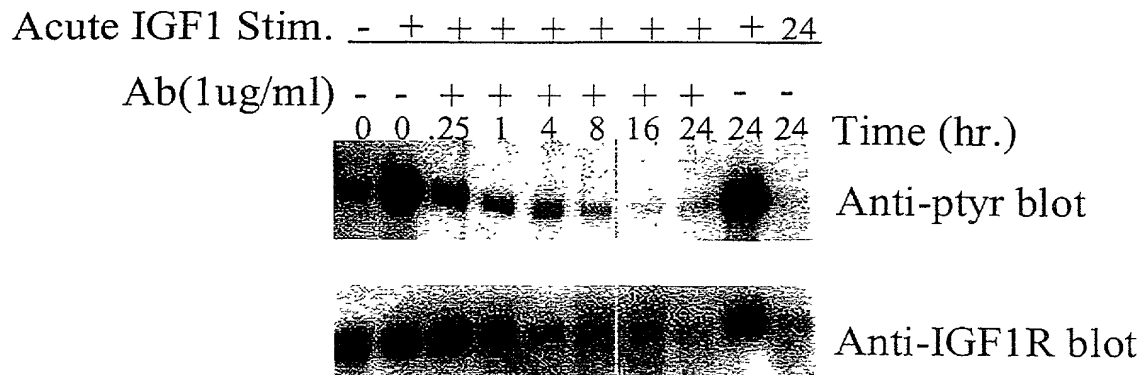


FIG. 4

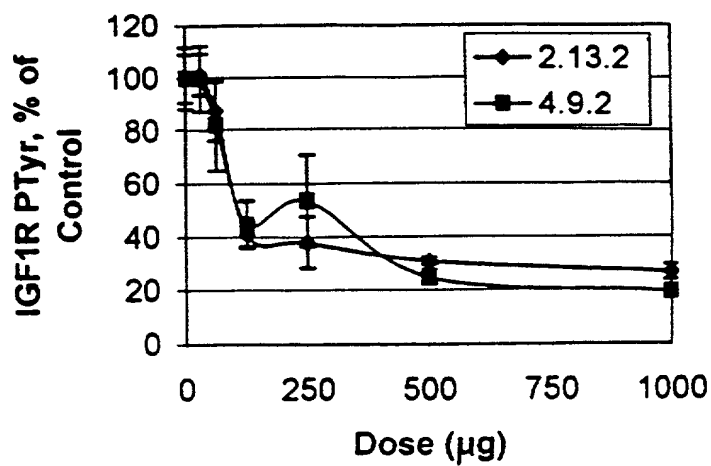


FIG. 5

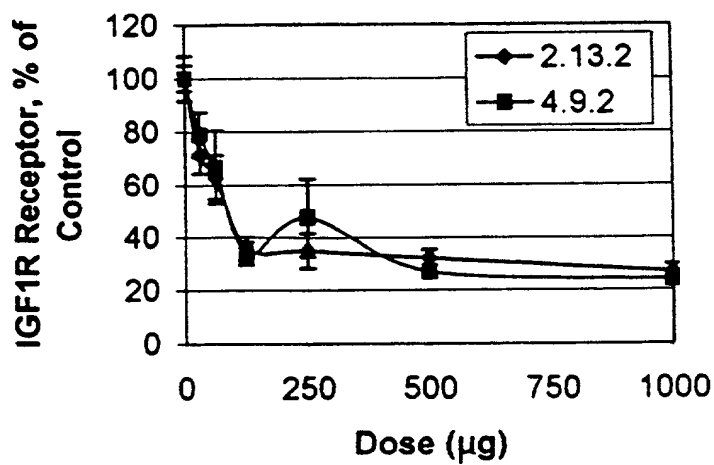
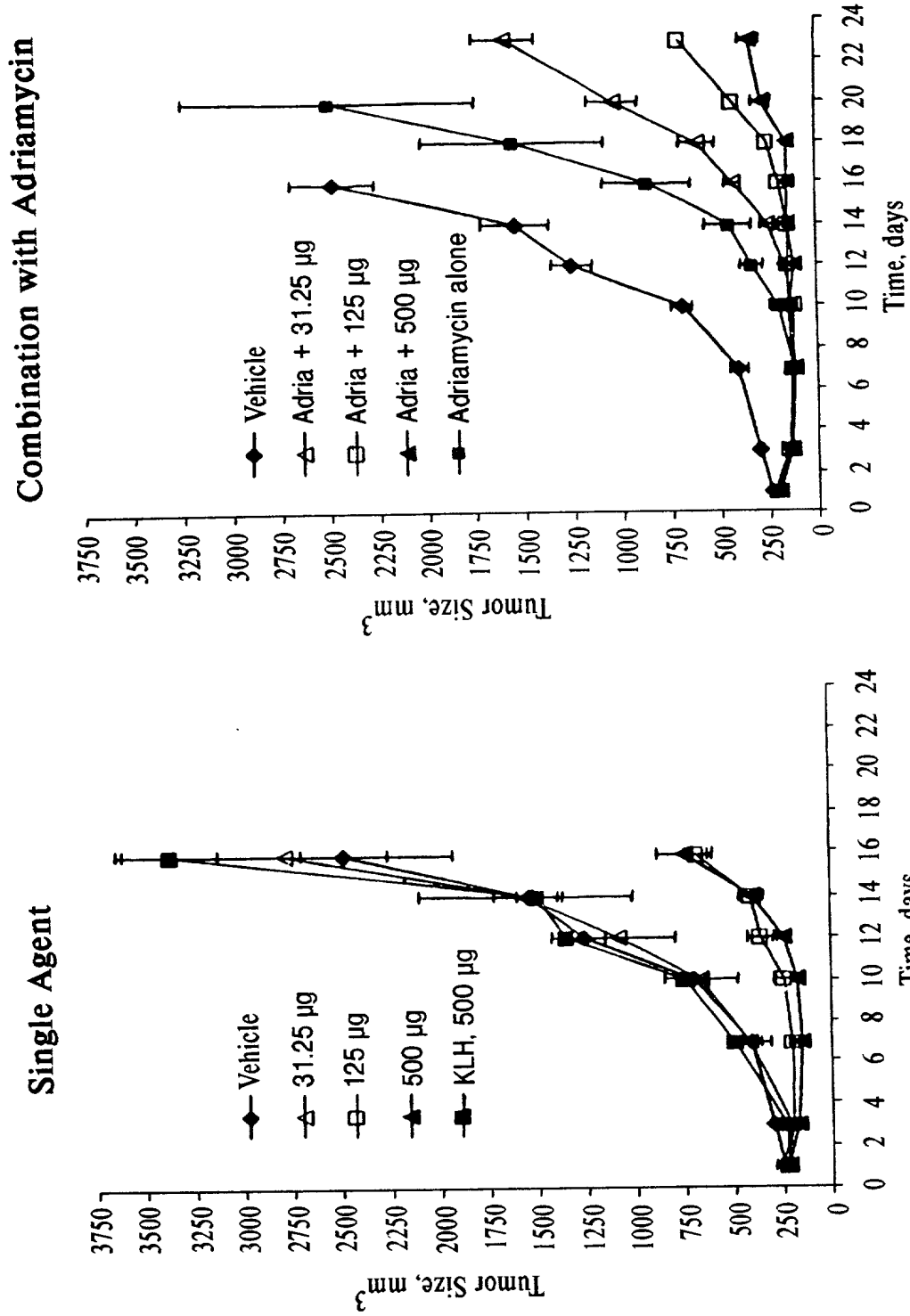


FIG. 6



Treatment: 125  $\mu$ g dose

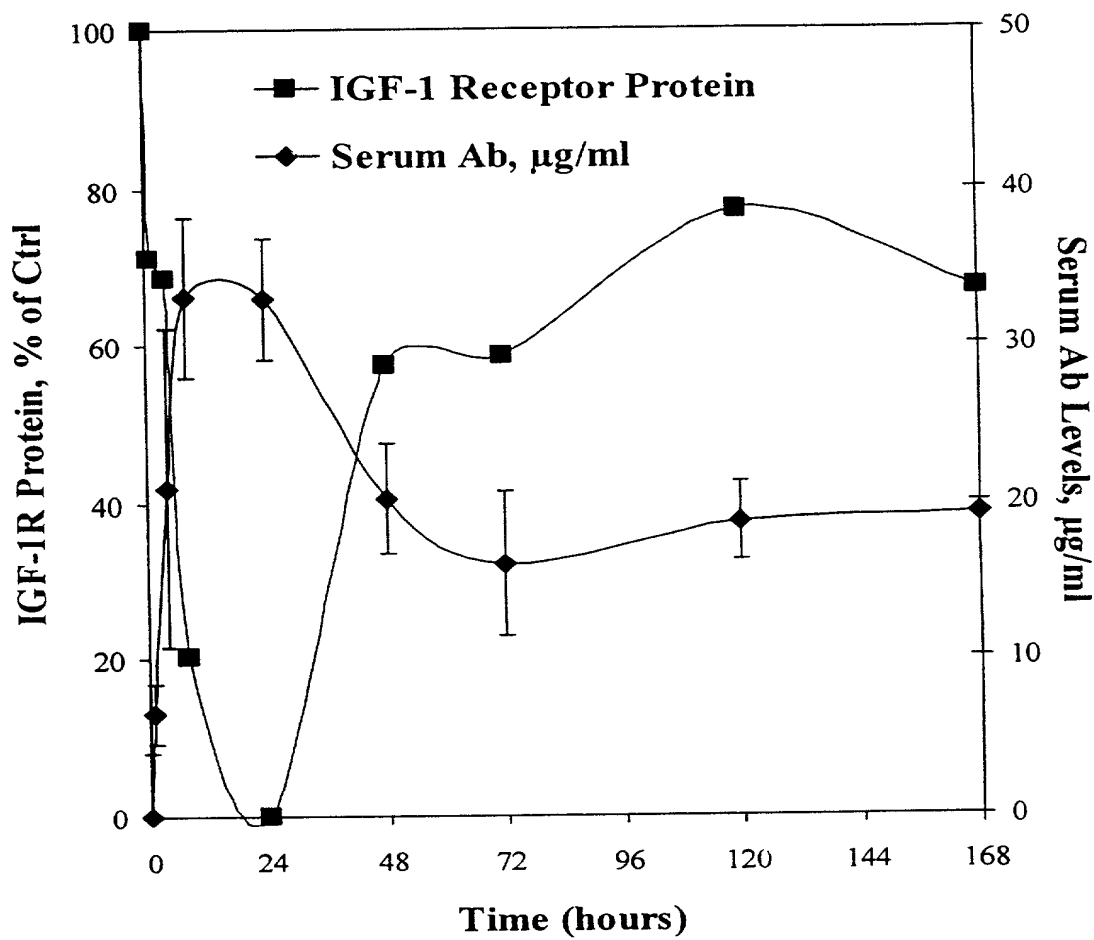


FIG. 8

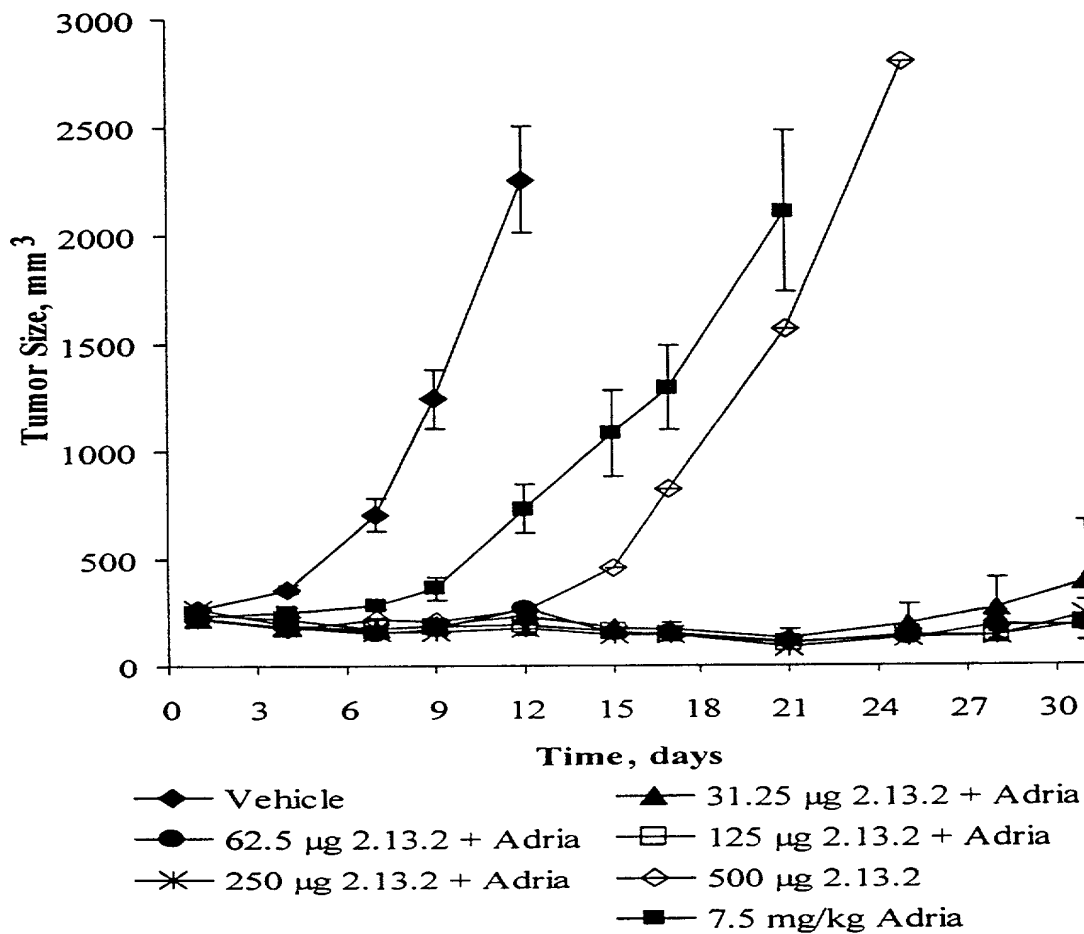


FIG. 9

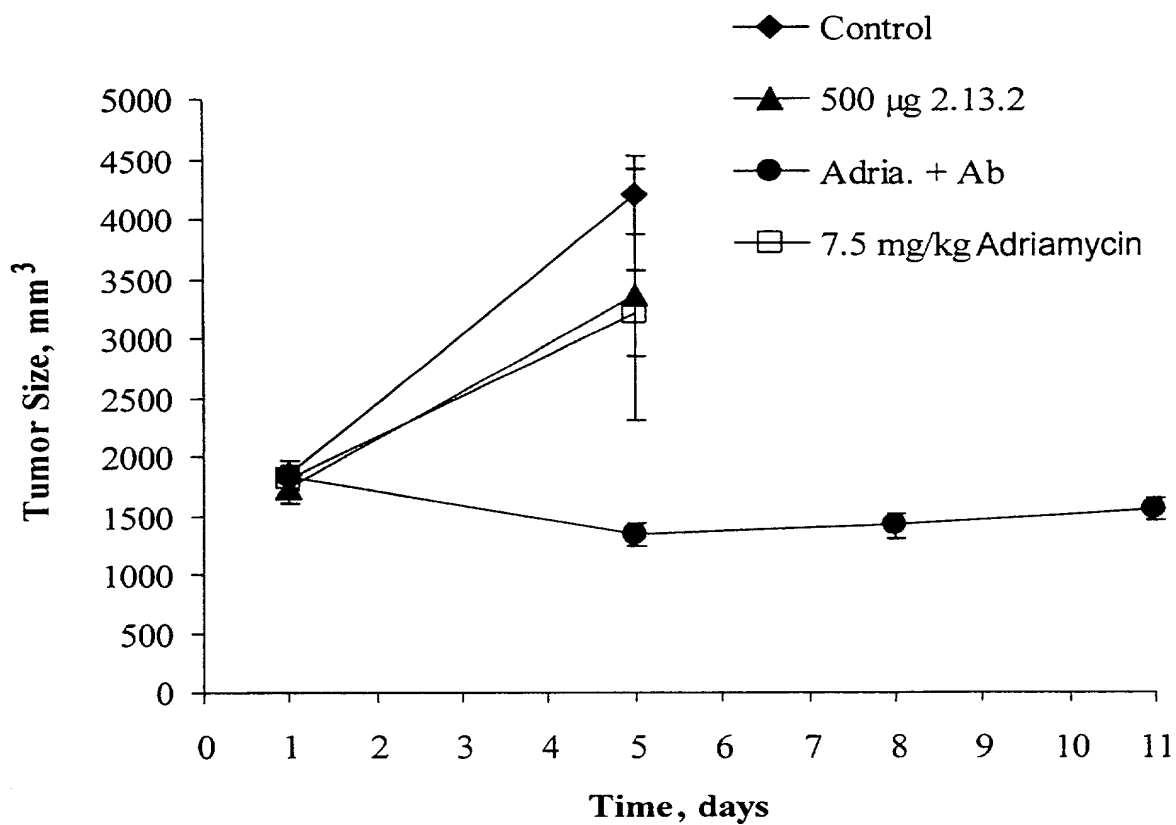


FIG. 10

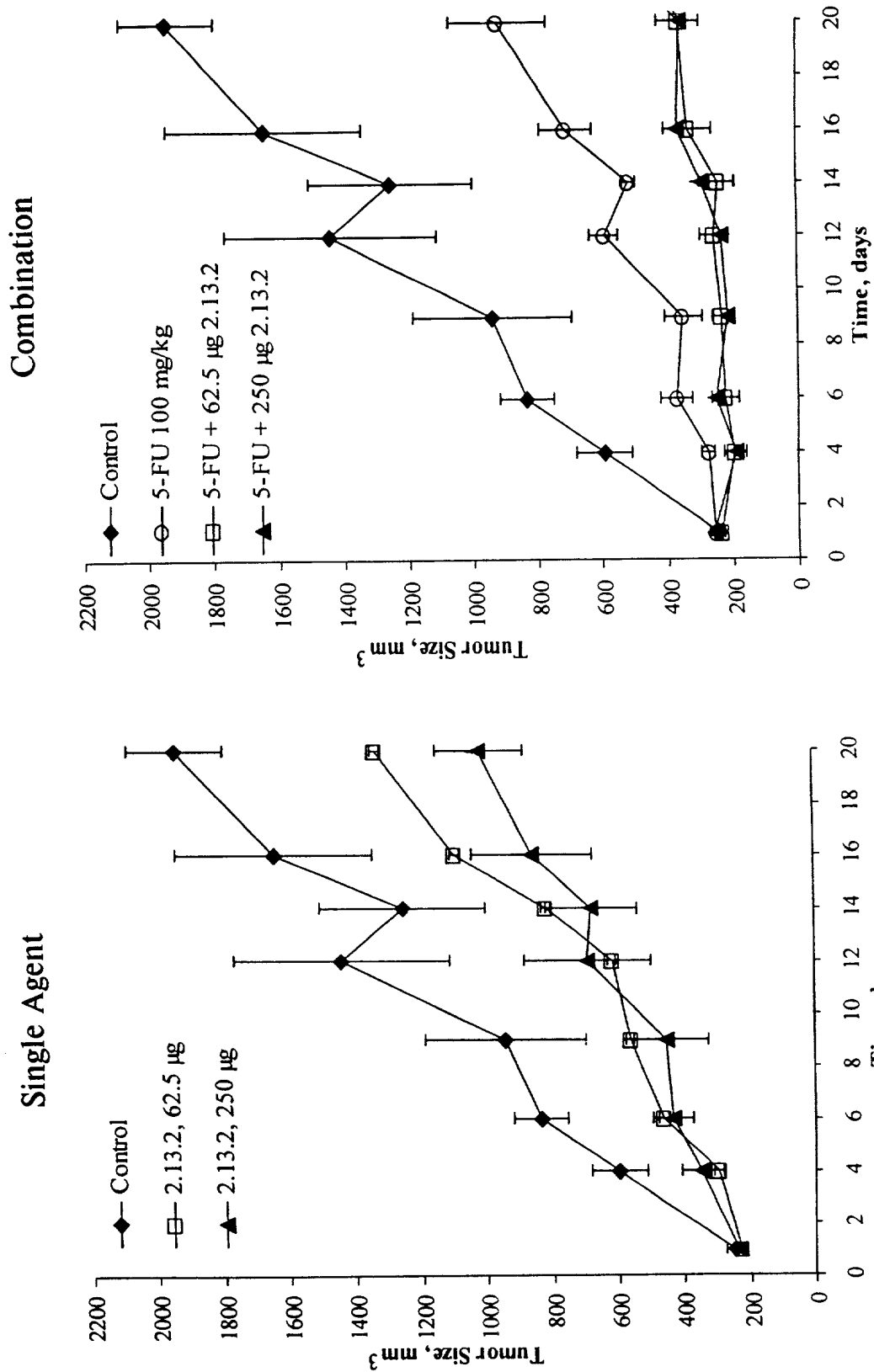


FIG. 11

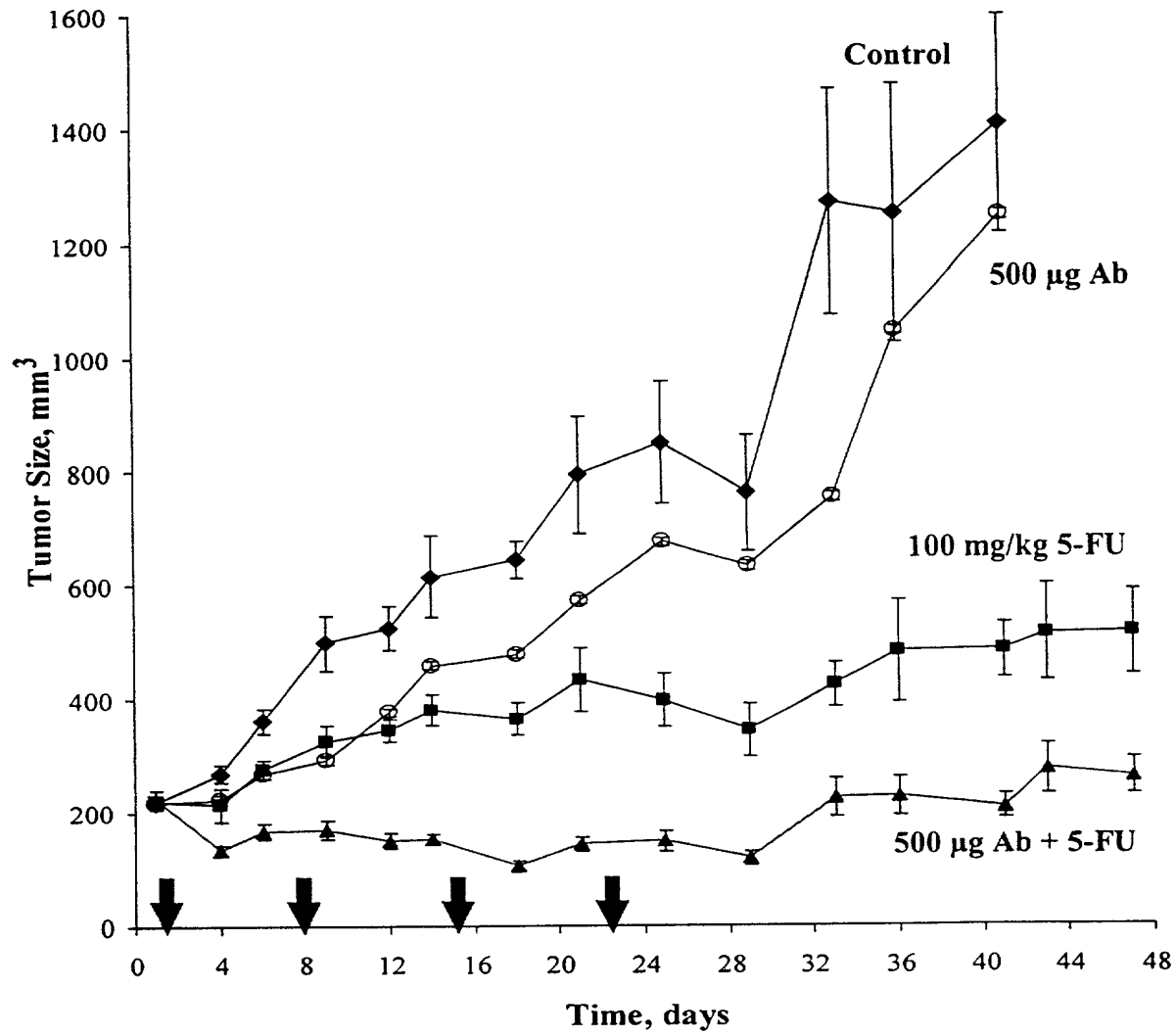


FIG. 12



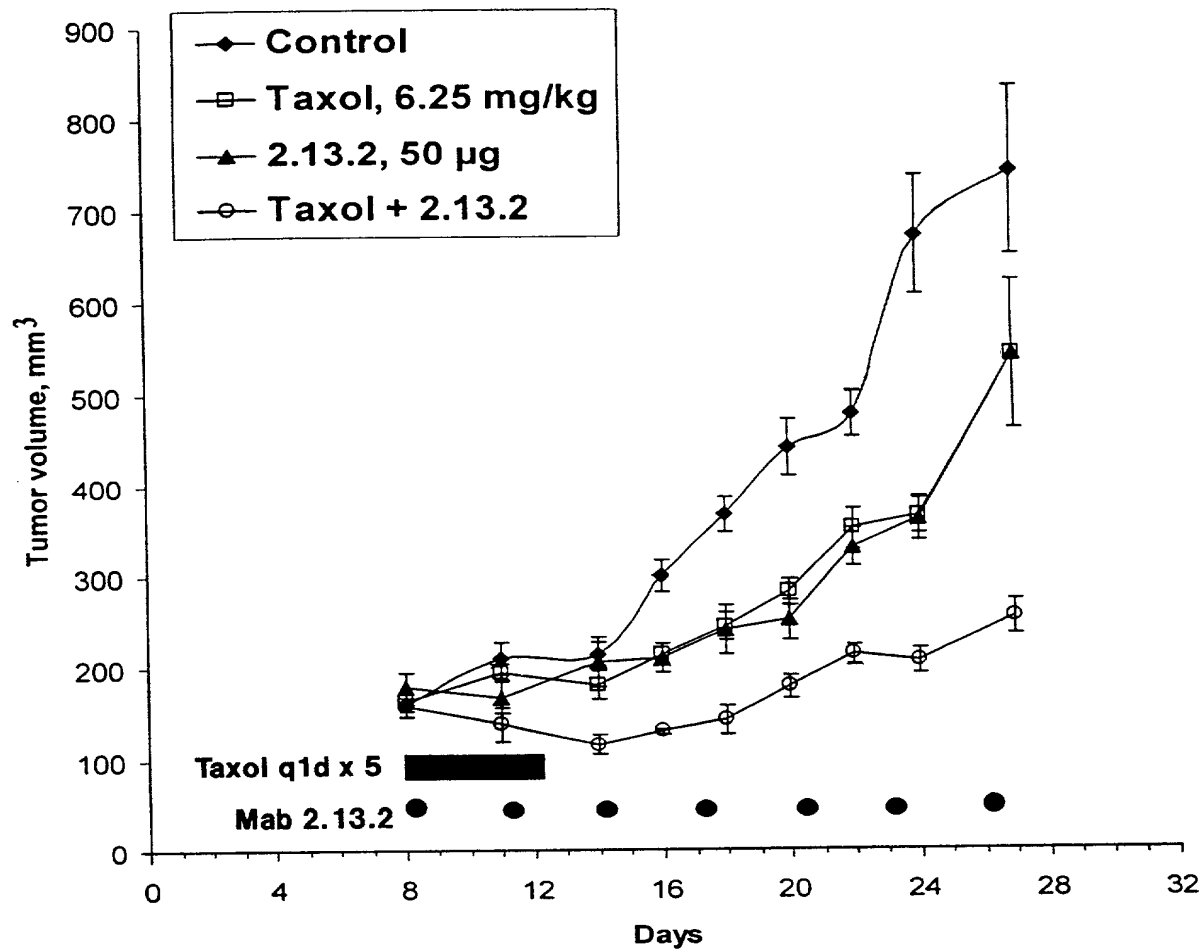
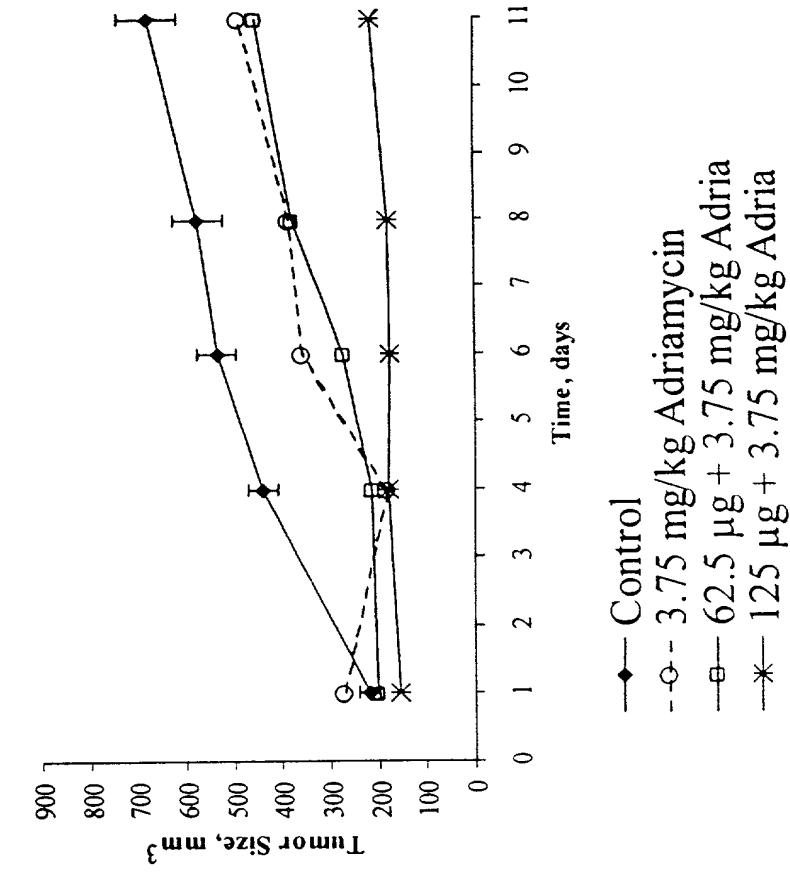


FIG. 13

## Combination



## Single Agent

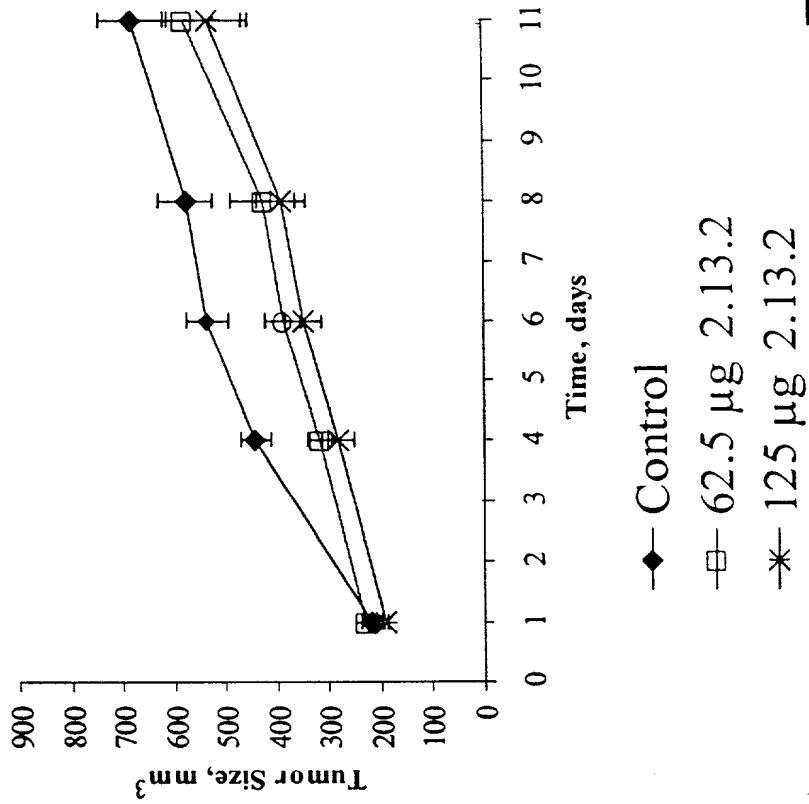
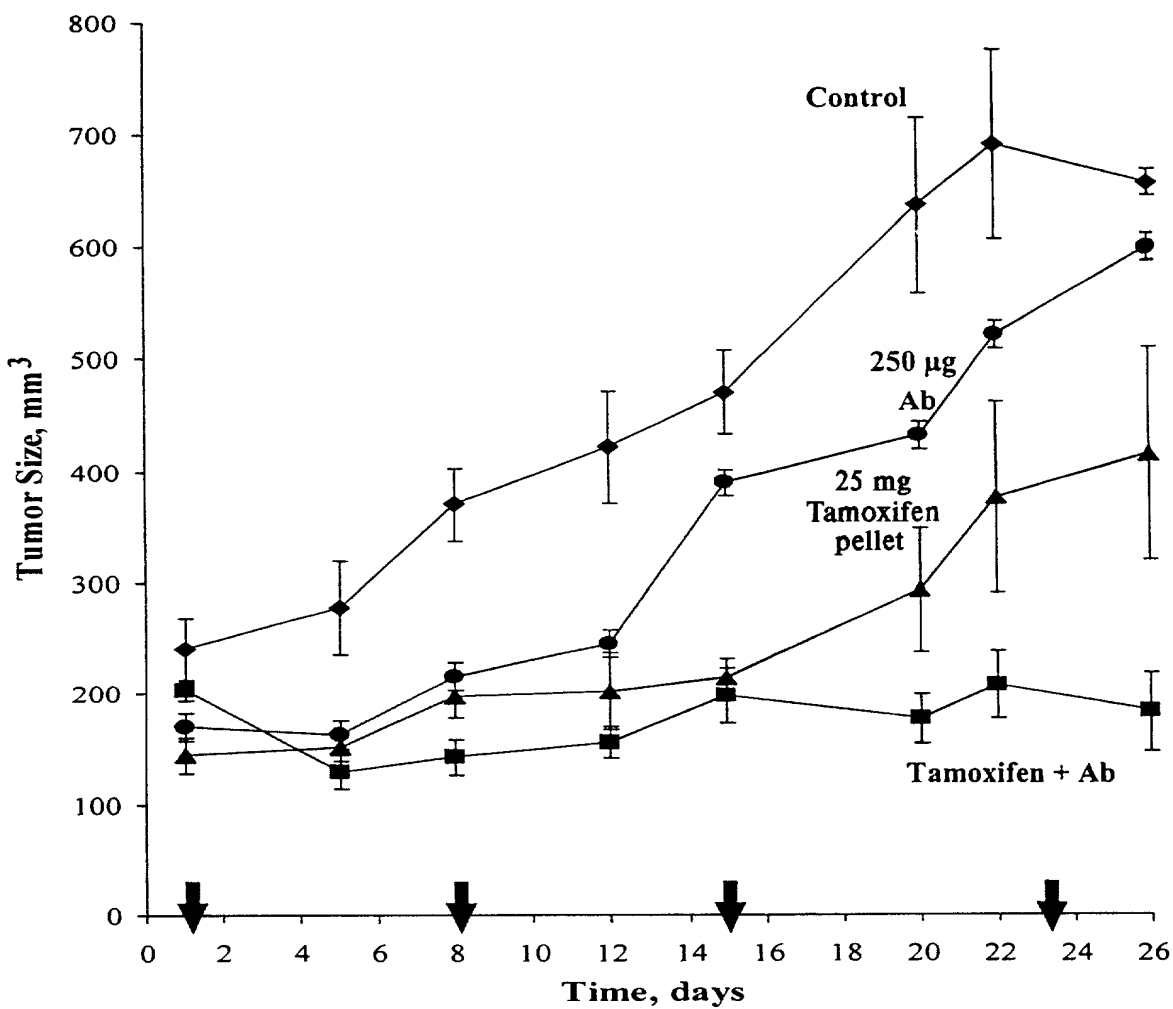


FIG. 14



**FIG. 15**

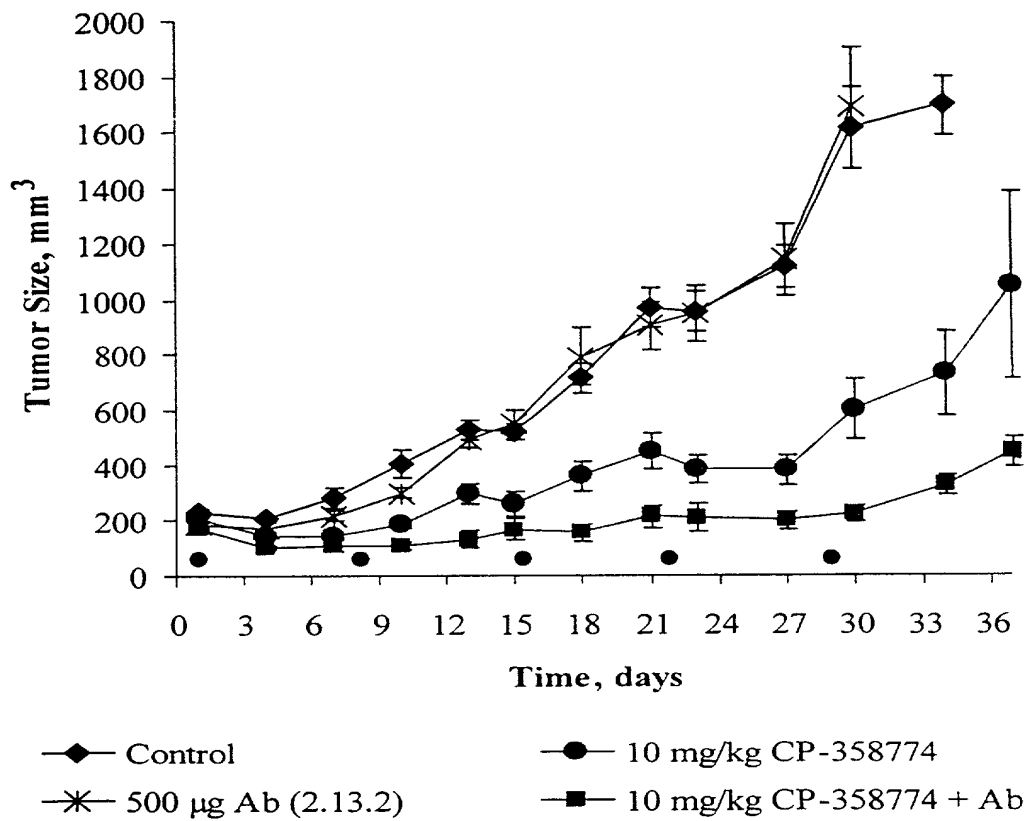


FIG. 16

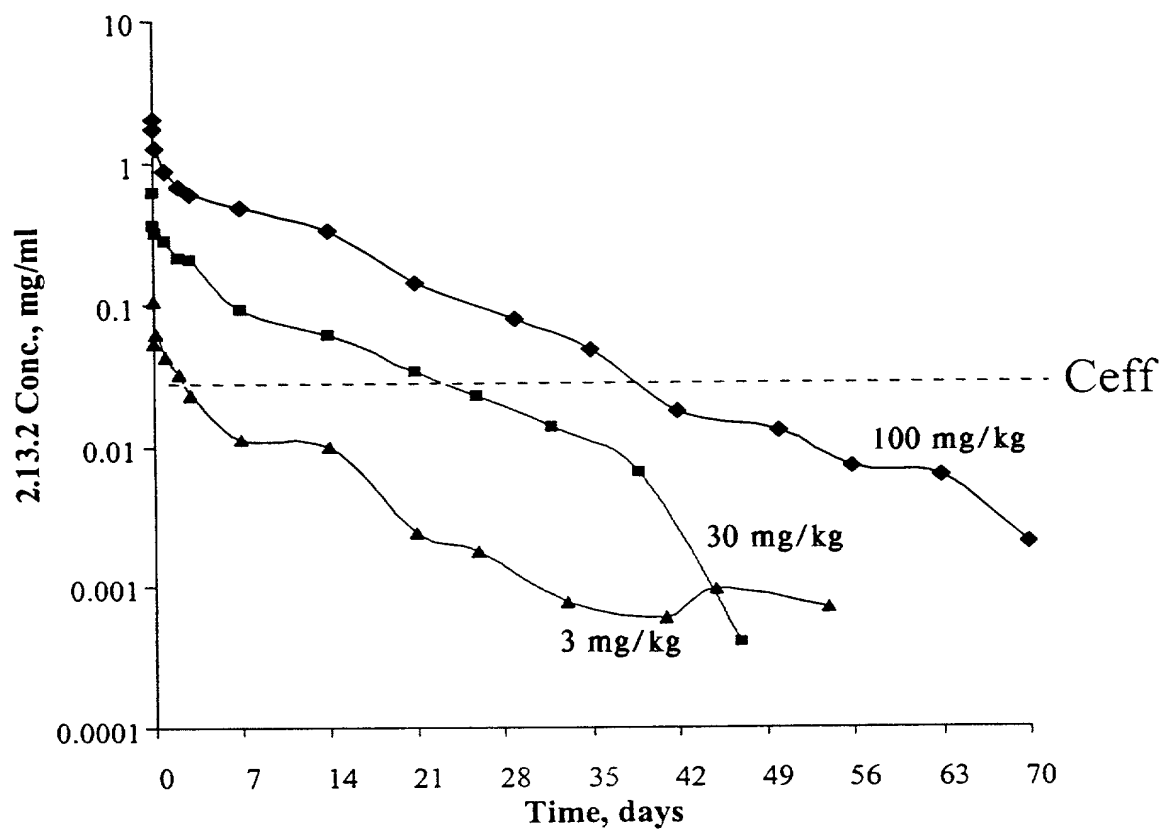


FIG. 17

Applicants:  
Application No.:  
For:  
Agent:

Bruce D. Cohen et al.  
To Be Assigned  
ANTIBODIES TO INSULIN-LIKE GROWTH  
FACTOR I RECEPTOR  
Karen E. Brown, Reg. No. 43,866

Docket No.: ABX-PF2 US  
Filed: Herewith  
Sheet 22 of 25

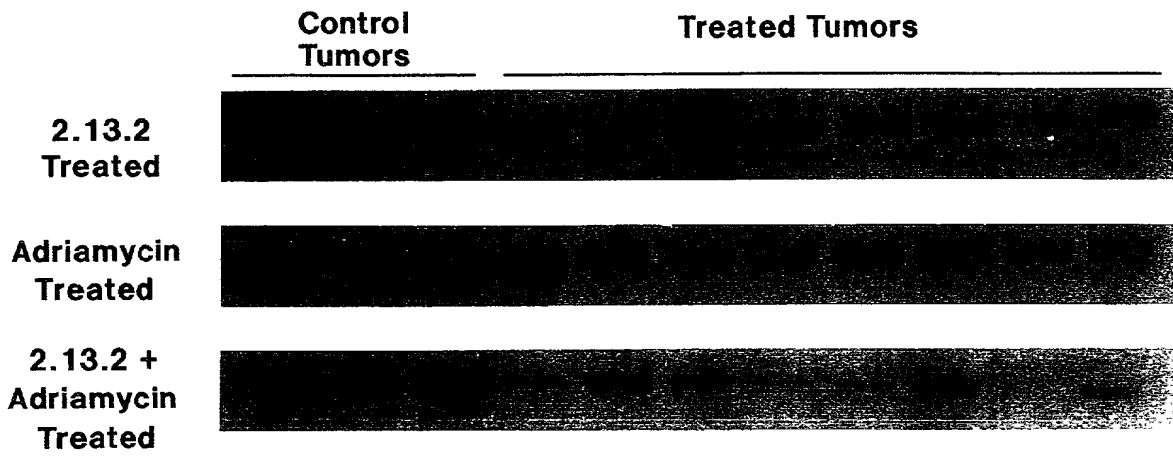


FIG. 18

Clone	C domain mutations	FR mutation	CDR mutation	Change in Cys	Change in glycosylation
2.13.2 Heavy	0	3	8	0	0
2.13.2 Light	0	1	4	1 (CDR3)	0
2.12.2 Heavy	0	2	8	0	0
2.12.2 Light	0	3	5	0	0

FIG. 19A

PF2 2.13.2 Heavy chain (DP-47(3-23)/D6-19/JH6) + \* \* \* \* \*

MEFGLSWLFL VAILKGVQCE VQLLESGLGL VQPGGSLRLS CTASGFTFS YAMNVRQAP GKGLEWVSAI SGGGTTFYA DSVKGRFTIS RDNSRTTLYL ++

MEFGLSWLFL VAILKGVQCE VQLLESGLGL VQPGGSLRLS CAASGFTFS YAMNVRQAP GKGLEWVSAI SGGGSTIYA DSVKGRFTIS RDNSKNTLYL

QMNSLRAEDT AVYYCAK--D LGWSDSYTY YGMDVWGQGT TTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP

QMNSLRAEDT AVYYCAKGYSGW--YTYTY YGMDVWGQGT TTVSSASTK GPSVFPLAPC SRSTSESTAA LGCLVKDYFP EPVTVSWNSG ALTSGVHTFP

AVLQSSGLYS LSSVTVTPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF

AVLQSSGLYS LSSVTVTPSS NFGTQTYTCN VDHKPSNTKV DKTVERKCCV ECPPCPAPPV AGPSVFLFPP KPKDTLMISR TPEVTCVVVD VSHEDPEVQF

NWYVDGVEVH NAKTKPREEQ FNSTFRVSV LTIVHQDWLN GKEYCKVSN KGLPAPIKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS

NWYVDGVEVH NAKTKPREEQ FNSTFRVSV LTIVHQDWLN GKEYCKVSN KGLPAPIKT ISKTKGQPRE PQVYTLPPSR EEMTKNQVSL TCLVKGFYPS

DIAVEWESNG OPENNYKTTT PMLDSDGSFF LYSKLTVDKS RMQGNVFSC SVMHEALHNNH YTKSLSLSP GK

DIAVEWESNG OPENNYKTTT PMLDSDGSFF LYSKLTVDKS RMQGNVFSC SVMHEALHNNH YTKSLSLSP GK

FIG. 19B

PF2 2.13.2 LC (A30/JK2)

MDMRVPAQLL GLLLLWFPGA RCDIQMTQFP + SLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAAASRLHRGV PSRFSGSGSG TEFTLTISSL  
MDMRVPAQLL GLLLLWFPGA RCDIQMTQSP \*\* SLSASVGDR VTITCRASQG IRNDLGWYQQ KPGKAPKRLI YAAASSLQSGV PSRFSGSGSG TEFTLTISSL

QPEDFATYYC LQHNSYPYTF GQGTGLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST  
QPEDFATYYC LQHNSYPYTF GQGTGLEIKR TVAAPSVFIF PPSDEQLKSG TASVVCCLNN FYPREAKVQW KVDNALQSGN SQESVTEQDS KDSTYSLSST

LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC  
LTLSKADYEK HKVYACEVTH QGLSSPVTKS FNRGEC

FIG. 19C

PF2 2.12.1 Heavy chain (DP-35 (3-11) /D3-3/JH6)

MEFGLSWVFL VAIKGVQCQ AQLVESGGGL VKPGGSLRLS CAASGFTFSD YMSWIRQAP GKGLEWVSYI SSSGSTRDYA DSVKGRFTIS RDNAKNSLYL  
MEFGLSWVFL VAIKGVQCQ VQLVESGGGL VKPGGSLRLS CAASGFTFSD YMSWIRQAP GKGLEWVSYI SSSGSTIYYA DSVKGRFTIS RDNAKNSLYL

QMNSLRARDT AVYICVR--D GVETTF-YYY YYGMDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF  
QMNSLRARDT AVYICARVLR FLEWLLYYYY YYGMDVWGQG TTVTVSSAST KGPSVFPLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF

PAVLQSSGLY SLSSVVTVPV SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ  
PAVLQSSGLY SLSSVVTVPV SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ

FNWYVDGVEV HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP  
FNWYVDGVEV HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK TISKTKGQPRE PQVYTLPPS REEMTKNQVS LTCLVKGFYP

SDIAYEWESN GQPENNYKTT PPMLDSGSGF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSLSP GK  
SDIAYEWESN GQPENNYKTT PPMLDSGSGF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN HYTKSLSLSP GK

FIG. 19D



PF2.12.1 Light chain (A30/Jk1)

MDMRVPAQLL	GLLLWFP	GA	RCDIQMTQSP	SSLSASVGDR	VTFTCRASQD	IRRDLGWYQQ	KPGKAPKRRLI	YAA SRLQSGV	PSRFSGSGSG	TEFTLTISSL
MDMRVPAQLL	GLLLWFP	GA	RCDIQMTQSP	SSLSASVGDR	VTITCRASQG	IRNDLGWYQQ	KPGKAPKRRLI	YAA SSLQSGV	PSRFSGSGSG	TEFTLTISSL
QPEDFATYYC	LQHNNYPRTF		GQGTEVEIIR	TVAAPSVFIF	PPSDEQLKSG	TASVVVCLLNN	FYPREAKVQW	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
QPEDFATYYC	LQHNSYPWTF		GQGTKVEIKR	TVAAPSVFIF	PPSDEQLKSG	TASVVVCLLNN	FYPREAKVQW	KVDNALQSGN	SQESVTEQDS	KDSTYSLSST
LTLSKADY EK	HKVYACEVTH		QGLSSPVTKS	FNRGEC						
LTLSKADY EK	HKVYACEVTH		QGLSSPVTKS	FNRGEC						

FIG. 19E